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TECH CENTER 1600/29

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<120> Nicotianamine Aminotransferase and Gene Therefor

<130> 2185-0226P

<140> 09/026,400
<141> 1998-02-19

<150> 09-037499 JAPAN
<151> 1997-02-21

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<170> PatentIn Ver. 2.0

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<220>
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  Met Val His Gln Ser Asn Gly His Gly Glu Ala Ala Ala Ala Ala Ala
    1   5   10   15

aac ggc aag agc aac ggg cac gcc gcc gcc gcg aac ggc aag agc aac   157
Asn Gly Lys Ser Asn Gly His Ala Ala Ala Ala Asn Gly Lys Ser Asn
            20   25   30

ggg cac gcg gcg gcg gcg gcg gtg gag tgg aat ttc gcc cgg ggc aag   205
Gly His Ala Ala Ala Ala Ala Val Glu Trp Asn Phe Ala Arg Gly Lys
            35   40   45

gac ggc atc ctg gcg acg acg ggg gcg aag aac agc atc cgg gcg ata   253
Asp Gly Ile Leu Ala Thr Thr Gly Ala Lys Asn Ser Ile Arg Ala Ile
    50   55   60

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cgg tac aag atc agc gcg agc gtg gag gag agc ggg ccg cgg ccc gtg   301
Arg Tyr Lys Ile Ser Ala Ser Val Glu Glu Ser Gly Pro Arg Pro Val
 65                  70                  75                  80

ctg ccg ctg gcc cac ggt gac ccg tcc gtg ttc ccg gcc ttc cgc acg   349
Leu Pro Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr
                 85                  90                  95

gcc gtc gag gcc gaa gac gcc gtc gcc gcc gcg ctg cgc acc ggc cag   397
Ala Val Glu Ala Glu Asp Ala Val Ala Ala Ala Leu Arg Thr Gly Gln
                100                 105                 110

ttc aac tgc tac gcc gcc ggc gtc ggc ctc ccc gcc gca cga agc gcc   445
Phe Asn Cys Tyr Ala Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala
            115                 120                 125

gta gca gag cac ttg tca cag ggc gtg ccc tac aag cta tcg gcc gac   493
Val Ala Glu His Leu Ser Gln Gly Val Pro Tyr Lys Leu Ser Ala Asp
        130                 135                 140

gac gtc ttc ctc acc gcc ggc gga act cag gcg atc gaa gtc ata atc   541
Asp Val Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile
145                 150                 155                 160

ccg gtg ctg gcc cag act gcc ggc gcc aac ata ctg ctt ccc cgg cca   589
Pro Val Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro
                165                 170                 175

ggc tat cca aat tac gag gcg cga gcg gca ttc aac aag ctg gag gtc   637
Gly Tyr Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Lys Leu Glu Val
                180                 185                 190

cgg cac ttc gac ctc atc ccc gac aag ggg tgg gag atc gac atc gac   685
Arg His Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp
            195                 200                 205

tcg ctg gaa tcc atc gcc gac aag aac acc acc gcg atg gtc atc ata   733
Ser Leu Glu Ser Ile Ala Asp Lys Asn Thr Thr Ala Met Val Ile Ile
        210                 215                 220

aac cca aac aat ccg tgc ggc agc gtt tac tcc tac gac cat ctg gcc   781
Asn Pro Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu Ala
225                 230                 235                 240

aag gtc gcg gag gtg gca agg aag ctc gga ata ttg gtg atc gct gac   829
Lys Val Ala Glu Val Ala Arg Lys Leu Gly Ile Leu Val Ile Ala Asp
                245                 250                 255
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2

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gag gtt tac ggc aaa ctg gtt ctg ggc agc gcc ccg ttt atc ccg atg      877
Glu Val Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro Met
            260             265             270

ggc gtc ttt ggg cac att gcc ccg gtc ttg tcc att gga tct ctg tcc      925
Gly Val Phe Gly His Ile Ala Pro Val Leu Ser Ile Gly Ser Leu Ser
            275             280             285

aag tcg tgg ata gtg cct gga tgg cga ctt gga tgg gtg gcg gtg tac      973
Lys Ser Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val Tyr
            290             295             300

gac ccc aca aag att tta gag aaa act aag atc tct acg tct att acg      1021
Asp Pro Thr Lys Ile Leu Glu Lys Thr Lys Ile Ser Thr Ser Ile Thr
305             310             315             320

aat tac ctt aat gtc tca acg gac cca gca acc ttc gtt cag gaa gct      1069
Asn Tyr Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Val Gln Glu Ala
            325             330             335

ctt cct aaa att ctt gag aac aca aaa gca gat ttc ttt aag agg att      1117
Leu Pro Lys Ile Leu Glu Asn Thr Lys Ala Asp Phe Phe Lys Arg Ile
            340             345             350

att ggt cta cta aag gaa tca tca gag ata tgt tat agg gaa ata aag      1165
Ile Gly Leu Leu Lys Glu Ser Ser Glu Ile Cys Tyr Arg Glu Ile Lys
            355             360             365

gaa aac aaa tat att acg tgt cct cac aag cca gaa gga tcg atg ttt      1213
Glu Asn Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met Phe
            370             375             380

gta atg gtc aaa cta aac tta cat ctt ttg gag gag atc cat gac gac      1261
Val Met Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile His Asp Asp
385             390             395             400

ata gat ttt tgc tgc aag ctc gca aag gaa gaa tca gta att tta tgt      1309
Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys
            405             410             415

cca ggg agt gtt ctt gga atg gaa aat tgg gtc cgt att act ttt gcc      1357
Pro Gly Ser Val Leu Gly Met Glu Asn Trp Val Arg Ile Thr Phe Ala
            420             425             430

tgc gtt cca tct tct ctt caa gat gga ctc gaa agg gtc aaa tca ttc      1405
Cys Val Pro Ser Ser Leu Gln Asp Gly Leu Glu Arg Val Lys Ser Phe
            435             440             445
```

3

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tgt caa agg aac aag aag aag aat tct ata aat ggt tgt ctagttgtaca      1454
Cys Gln Arg Asn Lys Lys Lys Asn Ser Ile Asn Gly Cys
    450                 455                 460


cacccctagt tgtacatctg actgaagctg taaatcattt ctagttatcc cccatttata 1514

tatttcaata aaacatattg taatggttct gttgtagctg tccaagtcat gtactctact 1574

ttttgatgta tttggcctca ttgccttgca tcaatttcaa taaaaatggt tgtgtacacc 1634

aaaaaaaaaa aaaaaaaaaa aaaaaa                                        1660
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<210> 2
<211> 461
<212> PRT
<213> Hordeum vulgare

<400> 2

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Met Val His Gln Ser Asn Gly His Gly Glu Ala Ala Ala Ala Ala Ala
 1               5                  10                  15

Asn Gly Lys Ser Asn Gly His Ala Ala Ala Ala Asn Gly Lys Ser Asn
            20                  25                  30

Gly His Ala Ala Ala Ala Ala Val Glu Trp Asn Phe Ala Arg Gly Lys
        35                  40                  45

Asp Gly Ile Leu Ala Thr Thr Gly Ala Lys Asn Ser Ile Arg Ala Ile
    50                  55                  60

Arg Tyr Lys Ile Ser Ala Ser Val Glu Glu Ser Gly Pro Arg Pro Val
65                  70                  75                  80

Leu Pro Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr
                85                  90                  95

Ala Val Glu Ala Glu Asp Ala Val Ala Ala Ala Leu Arg Thr Gly Gln
                100                 105                 110

Phe Asn Cys Tyr Ala Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala
            115                 120                 125

Val Ala Glu His Leu Ser Gln Gly Val Pro Tyr Lys Leu Ser Ala Asp
    130                 135                 140

Asp Val Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile
145                 150                 155                 160
```

4

Pro Val Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro
                165   170   175

Gly Tyr Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Lys Leu Glu Val
                180   185   190

Arg His Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp
                195   200   205

Ser Leu Glu Ser Ile Ala Asp Lys Asn Thr Thr Ala Met Val Ile Ile
        210   215   220

Asn Pro Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu Ala
225   230   235   240

Lys Val Ala Glu Val Ala Arg Lys Leu Gly Ile Leu Val Ile Ala Asp
                245   250   255

Glu Val Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro Met
                260   265   270

Gly Val Phe Gly His Ile Ala Pro Val Leu Ser Ile Gly Ser Leu Ser
                275   280   285

Lys Ser Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val Tyr
        290   295   300

Asp Pro Thr Lys Ile Leu Glu Lys Thr Lys Ile Ser Thr Ser Ile Thr
305   310   315   320

Asn Tyr Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Val Gln Glu Ala
                325   330   335

Leu Pro Lys Ile Leu Glu Asn Thr Lys Ala Asp Phe Phe Lys Arg Ile
                340   345   350

Ile Gly Leu Leu Lys Glu Ser Ser Glu Ile Cys Tyr Arg Glu Ile Lys
        355   360   365

Glu Asn Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met Phe
        370   375   380

Val Met Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile His Asp Asp
385   390   395   400

Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys
                405   410   415

5

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Pro Gly Ser Val Leu Gly Met Glu Asn Trp Val Arg Ile Thr Phe Ala
        420             425                 430

Cys Val Pro Ser Ser Leu Gln Asp Gly Leu Glu Arg Val Lys Ser Phe
        435             440                 445

Cys Gln Arg Asn Lys Lys Lys Asn Ser Ile Asn Gly Cys
    450             455                 460
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<210> 3
<211> 1910
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (76)..(1728)

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cctacccgtt tcctc atg gcc acc gta cgc cag agc gac gga gtc gcc gcg   111
                Met Ala Thr Val Arg Gln Ser Asp Gly Val Ala Ala
                  1               5                 10

aac ggc ctt gcc gtg gcc gca gcc gcg aac ggc aag agc aac ggc cat   159
Asn Gly Leu Ala Val Ala Ala Ala Ala Asn Gly Lys Ser Asn Gly His
            15              20                  25

ggc gtg gct gcc gcc gtg aac ggc aag agc aac ggc cat ggc gtg gat   207
Gly Val Ala Ala Ala Val Asn Gly Lys Ser Asn Gly His Gly Val Asp
        30              35                  40

gcc gac gcg aac ggc aag agc aac ggc cat ggc gtg gct gcc gac gcg   255
Ala Asp Ala Asn Gly Lys Ser Asn Gly His Gly Val Ala Ala Asp Ala
    45              50                  55              60

aac ggc aag agc aac ggc cat gcc gag gcc act gcg aac ggc cac ggc   303
Asn Gly Lys Ser Asn Gly His Ala Glu Ala Thr Ala Asn Gly His Gly
                65                  70                  75

gag gcc act gcg aac ggc aag acc aac ggc cac cgc gag agc aac ggc   351
Glu Ala Thr Ala Asn Gly Lys Thr Asn Gly His Arg Glu Ser Asn Gly
            80                  85                  90

cat gct gag gcc gcc gac gcg aac ggc gag agc aac gag cat gcc gag   399
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6

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                His Ala Glu Ala Ala Asp Ala Asn Gly Glu Ser Asn Glu His Ala Glu
                         95                  100                 105

gac tcc gcg gcg aac ggc gag agc aac ggg cat gcg gcg gcg gcg gca          447
Asp Ser Ala Ala Asn Gly Glu Ser Asn Gly His Ala Ala Ala Ala Ala
         110                 115                 120

gag gag gag gag gcg gtg gag tgg aat ttc gcg ggt gcc aag gac ggc          495
Glu Glu Glu Glu Ala Val Glu Trp Asn Phe Ala Gly Ala Lys Asp Gly
125                 130                 135                 140

gtg ctg gcg gcg acg ggg gcg aac atg agc atc cgg gcg ata cgg tac          543
Val Leu Ala Ala Thr Gly Ala Asn Met Ser Ile Arg Ala Ile Arg Tyr
                 145                 150                 155

aag atc agc gcg agc gtg cag gag aag ggg ccg cgg ccc gtg ctg ccg          591
Lys Ile Ser Ala Ser Val Gln Glu Lys Gly Pro Arg Pro Val Leu Pro
                 160                 165                 170

ctg gcc cac ggg gac ccg tcc gtg ttc ccg gcc ttc cgc acg gcc gtc          639
Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr Ala Val
                 175                 180                 185

gag gcc gag gac gcc gtc gcc gcc gcc gtg cgc acc ggc cag ttc aac          687
Glu Ala Glu Asp Ala Val Ala Ala Ala Val Arg Thr Gly Gln Phe Asn
         190                 195                 200

tgc tac ccc gcc ggc gtc ggc ctc ccc gcc gca cga agc gcc gtg gca          735
Cys Tyr Pro Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala Val Ala
205                 210                 215                 220

gag cac ctg tcg cag ggc gtg ccg tac atg cta tcg gcc gac gac gtc          783
Glu His Leu Ser Gln Gly Val Pro Tyr Met Leu Ser Ala Asp Asp Val
                 225                 230                 235

ttc ctc acc gcc ggc ggg acc cag gcg atc gag gtc ata atc ccg gtg          831
Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile Pro Val
                 240                 245                 250

ctg gcc cag acc gcc ggc gcc aac att ctg ctc ccc agg cca ggc tac          879
Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro Gly Tyr
                 255                 260                 265

cca aac tac gag gcg cgc gcc gcg ttc aac agg ctg gag gtc cgg cat          927
Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Arg Leu Glu Val Arg His
         270                 275                 280

ttc gac ctc atc ccc gac aag ggg tgg gag atc gac atc gac tcg ctg          975
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7

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Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp Ser Leu
285                 290                 295                 300


gaa tcc atc gcc gac aag aac acc acc gcc atg gtc atc ata aac ccc   1023
Glu Ser Ile Ala Asp Lys Asn Thr Thr Ala Met Val Ile Ile Asn Pro
                    305                 310                 315


aac aac ccg tgc ggc agc gtt tac tcc tac gac cat ctg tcc aag gtc   1071
Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu Ser Lys Val
                320                 325                 330


gcg gag gtg gcg aaa agg ctc gga ata ttg gtg att gct gac gag gta   1119
Ala Glu Val Ala Lys Arg Leu Gly Ile Leu Val Ile Ala Asp Glu Val
            335                 340                 345


tac ggc aag ctg gtt ctg ggc agc gcc ccg ttc atc cca atg gga gtg   1167
Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro Met Gly Val
            350                 355                 360


ttt ggg cac atc acc cct gtg ctg tcc ata ggg tct ctg tcc aag tca   1215
Phe Gly His Ile Thr Pro Val Leu Ser Ile Gly Ser Leu Ser Lys Ser
365                 370                 375                 380


tgg ata gtg cct gga tgg cgg ctt gga tgg gta gcg gtg tac gac ccc   1263
Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val Tyr Asp Pro
                385                 390                 395


aga aag atc tta cag gaa act aag atc tct aca tca att acg aat tac   1311
Arg Lys Ile Leu Gln Glu Thr Lys Ile Ser Thr Ser Ile Thr Asn Tyr
                400                 405                 410


ctc aat gtc tcg aca gac cca gca acc ttc att cag gca gct ctt cct   1359
Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Ile Gln Ala Ala Leu Pro
            415                 420                 425


cag att ctt gag aac aca aag gaa gat ttc ttt aag gcg att att ggt   1407
Gln Ile Leu Glu Asn Thr Lys Glu Asp Phe Phe Lys Ala Ile Ile Gly
        430                 435                 440


ctg cta aag gaa tca tca gag ata tgc tac aaa caa ata aag gaa aac   1455
Leu Leu Lys Glu Ser Ser Glu Ile Cys Tyr Lys Gln Ile Lys Glu Asn
445                 450                 455                 460


aaa tac att aca tgt cct cac aag cca gaa gga tca atg ttt gtc atg   1503
Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met Phe Val Met
                465                 470                 475


gtg aaa ctg aac tta cat ctt ttg gag gaa ata gac gat gac att gat   1551
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8

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Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile Asp Asp Asp Ile Asp
            480                 485                 490

ttt tgc tgc aag ctc gca aaa gaa gaa tca gta atc tta tgc cca ggg   1599
Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys Pro Gly
            495                 500                 505

agt gtt ctt gga atg gca aac tgg gtc cgc att act ttt gct tgt gtt   1647
Ser Val Leu Gly Met Ala Asn Trp Val Arg Ile Thr Phe Ala Cys Val
            510                 515                 520

cca tct tct ctt caa gat ggt ctc gga agg atc aaa tca ttc tgt caa   1695
Pro Ser Ser Leu Gln Asp Gly Leu Gly Arg Ile Lys Ser Phe Cys Gln
525                 530                 535                 540

agg aac aag aag aga aat tcg agc gat gat tgc tagttgtata tctgactgaa 1748
Arg Asn Lys Lys Arg Asn Ser Ser Asp Asp Cys
            545                 550

gctgtaaatc attcccagta tccccatcta tatctttcaa taaaatggaa cttttagttc 1808

tctatgaata gaagtcaaca tctccttgaa tatgttctgg ttgttgtggc ctggacgaaa 1868

catagtgaat gttatgttag tgaagttaaa aaaaaaaaaa aa                     1910


<210> 4
<211> 551
<212> PRT
<213> Hordeum vulgare

<400> 4
Met Ala Thr Val Arg Gln Ser Asp Gly Val Ala Ala Asn Gly Leu Ala
 1               5                  10                  15

Val Ala Ala Ala Ala Asn Gly Lys Ser Asn Gly His Gly Val Ala Ala
            20                  25                  30

Ala Val Asn Gly Lys Ser Asn Gly His Gly Val Asp Ala Asp Ala Asn
            35                  40                  45

Gly Lys Ser Asn Gly His Gly Val Ala Ala Asp Ala Asn Gly Lys Ser
        50                  55                  60

Asn Gly His Ala Glu Ala Thr Ala Asn Gly His Gly Glu Ala Thr Ala
65                  70                  75                  80

Asn Gly Lys Thr Asn Gly His Arg Glu Ser Asn Gly His Ala Glu Ala
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9

Ala Asp Ala Asn Gly Glu Ser Asn Glu His Ala Glu Asp Ser Ala Ala
            100   105   110

Asn Gly Glu Ser Asn Gly His Ala Ala Ala Ala Ala Glu Glu Glu Glu
            115   120   125

Ala Val Glu Trp Asn Phe Ala Gly Ala Lys Asp Gly Val Leu Ala Ala
        130   135   140

Thr Gly Ala Asn Met Ser Ile Arg Ala Ile Arg Tyr Lys Ile Ser Ala
145   150   155   160

Ser Val Gln Glu Lys Gly Pro Arg Pro Val Leu Pro Leu Ala His Gly
                165   170   175

Asp Pro Ser Val Phe Pro Ala Phe Arg Thr Ala Val Glu Ala Glu Asp
            180   185   190

Ala Val Ala Ala Ala Val Arg Thr Gly Gln Phe Asn Cys Tyr Pro Ala
        195   200   205

Gly Val Gly Leu Pro Ala Ala Arg Ser Ala Val Ala Glu His Leu Ser
    210   215   220

Gln Gly Val Pro Tyr Met Leu Ser Ala Asp Asp Val Phe Leu Thr Ala
225   230   235   240

Gly Gly Thr Gln Ala Ile Glu Val Ile Ile Pro Val Leu Ala Gln Thr
                245   250   255

Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro Gly Tyr Pro Asn Tyr Glu
            260   265   270

Ala Arg Ala Ala Phe Asn Arg Leu Glu Val Arg His Phe Asp Leu Ile
        275   280   285

Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp Ser Leu Glu Ser Ile Ala
    290   295   300

Asp Lys Asn Thr Thr Ala Met Val Ile Ile Asn Pro Asn Asn Pro Cys
305   310   315   320

Gly Ser Val Tyr Ser Tyr Asp His Leu Ser Lys Val Ala Glu Val Ala
            325   330   335

Lys Arg Leu Gly Ile Leu Val Ile Ala Asp Glu Val Tyr Gly Lys Leu

Val Leu Gly Ser Ala Pro Phe Ile Pro Met Gly Val Phe Gly His Ile
            355   360   365

Thr Pro Val Leu Ser Ile Gly Ser Leu Ser Lys Ser Trp Ile Val Pro
        370   375   380

Gly Trp Arg Leu Gly Trp Val Ala Val Tyr Asp Pro Arg Lys Ile Leu
385   390   395   400

Gln Glu Thr Lys Ile Ser Thr Ser Ile Thr Asn Tyr Leu Asn Val Ser
            405   410   415

Thr Asp Pro Ala Thr Phe Ile Gln Ala Ala Leu Pro Gln Ile Leu Glu
            420   425   430

Asn Thr Lys Glu Asp Phe Phe Lys Ala Ile Ile Gly Leu Leu Lys Glu
            435   440   445

Ser Ser Glu Ile Cys Tyr Lys Gln Ile Lys Glu Asn Lys Tyr Ile Thr
    450   455   460

Cys Pro His Lys Pro Glu Gly Ser Met Phe Val Met Val Lys Leu Asn
465   470   475   480

Leu His Leu Leu Glu Glu Ile Asp Asp Asp Ile Asp Phe Cys Cys Lys
            485   490   495

Leu Ala Lys Glu Glu Ser Val Ile Leu Cys Pro Gly Ser Val Leu Gly
            500   505   510

Met Ala Asn Trp Val Arg Ile Thr Phe Ala Cys Val Pro Ser Ser Leu
        515   520   525

Gln Asp Gly Leu Gly Arg Ile Lys Ser Phe Cys Gln Arg Asn Lys Lys
        530   535   540

Arg Asn Ser Ser Asp Asp Cys
545   550

<210> 5
<211> 23
<212> DNA
<213> Artificial Sequence

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<222> (1)..(23)
<223> n=inosine

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<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer 2

<220>
<221> modified_base
<222> (1)..(20)
<223> n=inosine

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gcdatrtgnc craanacncc   20

<210> 7
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:dt17 adapter
      primer

<400> 7
gactcgagtc gacatcgatt tttttttttt ttttt   35